

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 16, 2005, 15:48:46 ; Search time 177 Seconds

(without alignment)
454.217 Million cell updates/sec

Title: US-10-730-034-1

Sequence: 1 YFGLESKLSVIRNLNDQVL.....LKKEDELGDRSIMFTVQNE 157

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database: UniProt: 03:*

1: uniprot_sprot:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	811	99.9	189	2 Q6WUJ7	Q6WUJ7 homo sapien
2	811	99.9	193	1 IL18_HUMAN	Q1416 homo sapien
3	798	98.3	193	2 Q6KJ8	Q6KJ8 homo sapien
4	792	97.5	193	2 Q9B615	Q9B615 macaca mula
5	659	81.2	193	1 IL18_HORSE	Q9XQ7 equus caball
6	659	81.2	193	2 Q6T573	Q6T573 bubalus bub
7	654	80.5	178	2 Q6TLM4	Q6TLM4 bubalus bub
8	654	80.5	178	2 Q9MZL8	Q9MZL8 bos taurus
9	654	79.8	193	1 IL18_BOVIN	Q9TJ3 bos taurus
10	647	79.7	159	2 Q6GJ09	Q6GJ09 ovis aries
11	647	79.7	159	2 Q6QVCA	Q6QVCA capra hircu
12	637	78.4	192	1 IL18_PIG	Q19073 sus scrofa
13	634	78.1	192	2 Q9SM33	Q9SM33 felis silve
14	633	78.0	192	2 Q865B8	Q865B8 felis silve
15	626	77.1	192	2 Q9N1P7	Q9N1P7 sus scrofa
16	613	75.5	193	1 IL18_CANFA	Q9XK0 canis fami
17	578	71.2	177	2 Q6STL7	Q6STL7 sus scrofa
18	536.5	66.1	195	2 Q80T07	Q80T07 meriones un
19	515	63.4	189	2 Q80S58	Q80S58 mus musculu
20	515	63.4	192	1 IL18_MOUSE	P70380 mus musculu
21	514.5	63.4	194	1 IL18_RAT	P76366 rattus norv
22	501	61.7	192	2 Q6US06	Q6US06 mus musculu
23	441	54.3	196	2 Q91266	Q91266 bigmodon hi
24	313	38.5	84	2 Q951E7	Q951E7 canis fami
25	204	25.1	45	2 Q9NQ49	Q9NQ49 homo sapien
26	193	23.8	211	2 Q98S01	Q98S01 anas platyr
27	184.5	22.7	198	2 Q8AV26	Q8AV26 melagris g
28	182.5	22.5	169	2 Q61T44	Q61T44 gallus gall
29	182.5	22.5	198	2 Q918D2	Q918D2 gallus gall
30	178.5	22.0	196	1 IL18_CHICK	Q8Q18 gallus gall
31	116	14.3	199	2 Q70BK1	Q70BK1 oncorhynch

32	111	13.7	182	2 Q6EV48	Q6EV48 oncorhynch
33	111	13.7	199	2 Q6EV49	Q6EV49 oncorhynch
34	88	10.8	181	2 Q6F0J1	Q6F0J1 mesopliasma
35	88	10.8	4705	1 FAT2_DROME	Q9VW71 droscophila
36	86.5	10.7	376	2 Q8K4E6	Q8K4E6 mus musculu
37	86.5	10.7	376	2 Q8K4E7	Q8K4E7 mus musculu
38	85.5	10.5	867	2 Q7RNN8	Q7RNN8 plasmodium
39	85	10.5	252	2 Q8JZM4	Q8JZM4 mus musculu
40	84.5	10.4	376	2 Q8K4E8	Q8K4E8 mus musculu
41	84	10.3	1101	2 Q6C1C3	Q6C1C3 kluyveromyc
42	83.5	10.3	182	2 Q430J1	Q430J1 schizosacch
43	83.5	10.3	454	2 Q8H2U5	Q8H2U5 tonatia sau
44	83.5	10.3	454	2 Q8H2U6	Q8H2U6 tonatia sau
45	83.5	10.3	454	2 Q8H2U7	Q8H2U7 tonatia sau

ALIGNMENTS

RESULT 1

ID	Q6WUJ7	PRELIMINARY:	PRT:	189 AA.
AC	Q6WUJ7			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	DELTA3PRO-IL-18.			
GN	Name=IL18.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Gageteo A., De Ambrosio A., Mezzanzanica D., Piazza T., Rubartelli A.,			
RA	Fidini M., Canavari S., Ferrini S.,			
RT	"A novel isoform of pro-interleukin-18 expressed in ovarian tumors is			
RT	resistant to caspase-1 and -4 processing.";			
RL	Oncogene 0:0-0(2004).			
DR	EMBL, AY26351; AAB92112.1; -			
DR	InterPro, IPR008996; Cytok_IL11ike.			
SQ	SEQUENCE 189 AA; 2189 MW; AABA275CF713A4B6 CRC64;			
Query Match				
Best Local Similarity 99.4%; Score 811; DB 2; Length 189;				
Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
QY	1 YFGLESKLSVIRNLNDQVLFDIDGNRPLFEDMTSDCDRNAPRTFIISMYKSOQPRGM 60			
DB	33 YFGLESKLSVIRNLNDQVLFDIDGNRPLFEDMTSDCDRNAPRTFIISMYKSOQPRGM 92			
QY	61 AVTISVKEKTSXKSCENKIISPKENMPDNIKOTKSDIIFFORSVPGHDNMQPESSTY 120			
DB	93 AVTISVKEKTSXKSCENKIISPKENMPDNIKOTKSDIIFFORSVPGHDNMQPESSTY 152			
QY	121 EGYFLACEKRDLPFLILKKEDELGDRSIMFTVQNE 157			
DB	153 EGYFLACEKRDLPFLILKKEDELGDRSIMFTVQNE 189			
RESULT 2				
ID	IL18_HUMAN	STANDARD;	PRT;	193 AA.
AC	Q1416; 075599;			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Interleukin-18 precursor (IL-18) (interferon-gamma inducing factor)			
DE	(IFN-gamma-inducing factor) (interleukin-1 gamma) (IL-1 gamma).			
GN	Name=IL18; Synonyms=IGIF;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			

NCBI_TaxID=9606;
 (1) SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=96247646; PubMed=8666798;
 RA Uehio S., Namba M., Okura T., Hattori K., Nakada Y., Akita K.,
 Tanabe F., Konishi K., Micallef M., Fujii M., Toriige K., Tanimoto T.,
 Fukuda S., Ikeda M., Okamura H., Kurimoto M.;
 RT "Cloning of the cDNA for human IFN-gamma-inducing factor, expression
 in Escherichia coli, and studies on the biologic activities of the
 protein.";
 RL J. Immunol. 156:4274-4279 (1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Yong D., Guixin D., Lihua H., Haitao W.;
 RT "Cloning and sequencing of the cDNA for precursor hIL-18";
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Liu J., Peng X., Yuan J., Qiang B.;
 RT "Cloning of human interleukin 18 cDNA";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Urinary bladder;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins P.S., Wagner L., Shennan C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heist F.,
 Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,
 Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millamy S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Villalón D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 Richardson D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Rutherford J.S., Krzywicki M.I., Skalska U., Smalins D.E.,
 Schenker A., Schein J.E., Jones S.J.M., Marra M.A.;
 RA "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RL [5]
 RN SEQUENCE OF 2-193 FROM N.A.
 RP TISSUE=Peripheral blood;
 RC Cont. B., Kim S.J., Tinti C., Chun H.S., Joh T.H.;
 RA Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RL -1- FUNCTION: Augments natural killer cell activity in spleen cells
 CC and stimulates interferon gamma production in T helper type I
 CC cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the IL-1 family.
 CC
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 CC
 CC EMBL; DA9950; BAA08706.1; -
 DR EMBL; AF077611; AAC27787.1; -
 DR EMBL; AY044641; AAC95950.1; -
 DR EMBL; BC007007; AAH07007.1; -
 DR EMBL; BC007461; AAH07461.1; -
 DR EMBL; U90434; AAB50010.1; -
 DR PDB; 1J0S; NMR; A=37-193.
 DR OGP; Q14116; -

DR Genew; H9NC:5986; IL18.
 DR H-InvDB; HIX0010123; -
 DR MIM; 600953; -
 DR GO; GO:0005576; C:extracellular; TAS.
 DR GO; GO:0005125; P:cytokine activity; TAS.
 DR GO; GO:0004871; P:signal transducer activity; TAS.
 DR GO; GO:0001525; P:angiogenesis; IDA.
 DR GO; GO:0007267; P:cell-cell signalling; TAS.
 DR GO; GO:0042033; P:chemokine biosynthesis; TAS.
 DR GO; GO:0042104; P:positive regulation of activated T-cell pro. .; IDA.
 DR GO; GO:0030155; P:regulation of cell adhesion; IDA.
 DR GO; GO:0030431; P:sleep; ISS.
 DR GO; GO:0042092; P:T-helper 2 type immune response; TAS.
 DR InterPro; IPR008996; CytoK_IL1-like.
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 KW 3D-structure; Cytokine.
 FT PROPEP 1 36 By similarity.
 FT CHAIN 37 193 Interleukin-18.
 FT CONFLICT 66 66 F -> L (in Ref. 2).
 FT CONFLICT 86 86 S -> R (in Ref. 2).
 FT CONFLICT 191 191 N -> S (in Ref. 2).
 SQ SEQUENCE 193 AA; 22326 MW; 323C62C203788D55 CRC64;
 Query Match 99.9%; Score 811; DB 1; Length 193;
 Blast Local Similarity 99.4%; Pred. No. 1.6e-67;
 Matches 156; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 YFGKLESLSYVRINADPVLFDQGNRPLEFEDMTSDCRDNAPRTIFISWYKDSQPRGM 60
 DB 37 YFGKLESLSYVRINADPVLFDQGNRPLEFEDMTSDCRDNAPRTIFISWYKDSQPRGM 96
 QY 61 AVTISVCKEKLISXLSGKNIISFKEMNPDPNIKOTXSIIFFQRSVPGHDKMGESESSY 120
 DB 97 AVTISVCKEKLISXLSGKNIISFKEMNPDPNIKOTXSIIFFQRSVPGHDKMGESESSY 156
 QY 121 EGYFLACEKRDLPFLILIKKEDELDGRSIFMTQVED 157
 DB 157 EGYFLACEKRDLPFLILIKKEDELDGRSIFMTQVED 193
 RESULT 3
 Q96KJ8 PRELIMINARY; PRT; 193 AA.
 AC Q96KJ8;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Interleukin 18.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ying P., Jianxin L.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF380360; AAK57024.1; -
 DR HSSP; Q14116; 1J0S.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005149; P:interleukin-1 receptor binding; IEA.
 DR GO; GO:0006945; P:immune response; IEA.
 DR InterPro; IPR008996; CytoK_IL1-like.
 DR InterPro; IPR000975; Interleukin_1.
 DR SMART; SM00125; IL1; 1.
 SQ SEQUENCE 193 AA; 22323 MW; 2E500205D1B7E5F7 CRC64;